

[illegible]

45

GGACACGGTG	CGCTTGGCAA	AGTGAAACCC	CAACAGAGAG	GCGAAAGCGA	GCCAAGACAC		60									
ACCACATACA	CACGAAGAGA	ACGAGCAAGA	AGAAACCGGT	AGGCGGAGGA	GGCGCTGCCC		120									
CCAGTTCCTC	CAATATACCC	AGCACCACAT	CACAAGCCCC	GG	ATG GAC AAC TGC		174									
					Met Asp Asn Cys											
					1											
GAC Asp 5	CAG Gln	GAC Asp	GCC Ala	AGC Ser	TTT Phe 10	CGG Arg	CTG Leu	AGC Ser	CAC His	ATC Ile 15	AAG Lys	GAG Glu	GAG Glu	GTC Val	AAG Lys 20	222
CCG Pro	GAC Asp	ATC Ile	TCG Ser	CAG Gln 25	CTG Leu	AAC Asn	GAC Asp	AGC Ser	AAC Asn 30	AGC Ser	AGC Ser	TTT Phe	TCG Ser 35	CCC Pro		270
AAG Lys	GCC Ala	GAG Glu	AGT Ser 40	CCC Pro	GTG Val	CCC Pro	TTC Phe	ATG Met 45	CAG Gln	GCC Ala	ATG Met	TCC Ser	ATG Met 50	GTC Val	CAC His	318
GTG Val	CTG Leu	CCC Pro 55	GGC Gly	TCC Ser	AAC Asn	TCC Ser	GCC Ala 60	AGC Ser	TCC Ser	AAC Asn	AAC Asn	AAC Asn 65	AGC Ser	GCT Ala	GGA Gly	366
GAT Asp	GCC Ala 70	CAA Gln	ATG Met	GCG Ala	CAG Gln	GCG Ala 75	CCC Pro	AAT Asn	TCG Ser	GCT Ala	GGA Gly 80	GGC Gly	TCT Ser	GCC Ala	GCC Ala	414
GCT Ala 85	GCA Ala	GTC Val	CAG Gln	CAG Gln	CAG Gln 90	TAT Tyr	CCG Pro	CCT Pro	AAC Asn	CAT His 95	CCG Pro	CTG Leu	AGC Ser	GGC Gly	AGC Ser 100	462
AAG Lys	CAC His	CTC Leu	TGC Cys	TCT Ser 105	ATT Ile	TGC Cys	GGG Gly	GAT Asp	CGG Arg 110	GCC Ala	AGT Ser	GGC Gly	AAG Lys	CAC His 115	TAC Tyr	510
GGC Gly	GTG Val	TAC Tyr	AGC Ser 120	TGT Cys	GAG Glu	GGC Gly	TGC Cys	AAG Lys 125	GGC Gly	TTC Phe	TTT Phe	AAA Lys	CGC Arg 130	ACA Thr	GTG Val	558
CGC Arg	AAG Lys	GAT Asp 135	CTC Leu	ACA Thr	TAC Tyr	GCT Ala	TGC Cys 140	AGG Arg	GAG Glu	AAC Asn	CGC Arg	AAC Asn 145	TGC Cys	ATC Ile	ATA Ile	606
GAC Asp	AAG Lys 150	CGG Arg	CAG Gln	AGG Arg	AAC Asn	CGC Arg 155	TGC Cys	CAG Gln	TAC Tyr	TGC Cys	CGC Arg 160	TAC Tyr	CAG Gln	AAG Lys	TGC Cys	654
CTA Leu 165	ACC Thr	TGC Cys	GGC Gly	ATG Met	AAG Lys 170	CGC Arg	GAA Glu	GCG Ala	GTC Val	CAG Gln 175	GAG Glu	GAG Glu	CGT Arg	CAA Gln	CGC Arg 180	702
GGC Gly	GCC Ala	CGC Arg	AAT Asn	GCG Ala 185	GCG Ala	GGT Gly	AGG Arg	CTC Leu	AGC Ser 190	GCC Ala	AGC Ser	GGA Gly	GGC Gly	GGC Gly 195	AGT Ser	750
AGC Ser	GGT Gly	CCA Pro	GGT Gly 200	TCG Ser	GTA Val	GGC Gly	GGA Gly	TCC Ser 205	AGC Ser	TCT Ser	CAA Gln	GGC Gly	GGA Gly 210	GGA Gly	GGA Gly	798

GGA	GGC	GGC	GTT	TCT	GGC	GGA	ATG	GGC	AGC	GGC	AAC	GGT	TCT	GAT	GAC	846
Gly	Gly	Gly	Val	Ser	Gly	Gly	Met	Gly	Ser	Gly	Asn	Gly	Ser	Asp	Asp	
		215					220					225				
TTC	ATG	ACC	AAT	AGC	GTG	TCC	AGG	GAT	TTC	TCG	ATC	GAG	CGC	ATC	ATA	894
Phe	Met	Thr	Asn	Ser	Val	Ser	Arg	Asp	Phe	Ser	Ile	Glu	Arg	Ile	Ile	
	230					235					240					
GAG	GCC	GAG	CAG	CGA	GCG	GAG	ACC	CAA	TGC	GGC	GAT	CGT	GCA	CTG	ACG	942
Glu	Ala	Glu	Gln	Arg	Ala	Glu	Thr	Gln	Cys	Gly	Asp	Arg	Ala	Leu	Thr	
245					250					255					260	
TTC	CTG	CGC	GTT	GGT	CCC	TAT	TCC	ACA	GTC	CAG	CCG	GAC	TAC	AAG	GGT	990
Phe	Leu	Arg	Val	Gly	Pro	Tyr	Ser	Thr	Val	Gln	Pro	Asp	Tyr	Lys	Gly	
				265					270					275		
GCC	GTG	TCG	GCC	CTG	TGC	CAA	GTG	GTC	AAC	AAA	CAG	CTC	TTC	CAG	ATG	1038
Ala	Val	Ser	Ala	Leu	Cys	Gln	Val	Val	Asn	Lys	Gln	Leu	Phe	Gln	Met	
			280					285					290			
GTC	GAA	TAC	GCG	CGC	ATG	ATG	CCG	CAC	TTT	GCC	CAG	GTG	CCG	CTG	GAC	1086
Val	Glu	Tyr	Ala	Arg	Met	Met	Pro	His	Phe	Ala	Gln	Val	Pro	Leu	Asp	
		295					300					305				
GAC	CAG	GTG	ATT	CTG	CTG	AAA	GCC	GCT	TGG	ATC	GAG	CTG	CTC	ATT	GCG	1134
Asp	Gln	Val	Ile	Leu	Leu	Lys	Ala	Ala	Trp	Ile	Glu	Leu	Leu	Ile	Ala	
	310					315					320					
AAC	GTG	GCC	TGG	TGC	AGC	ATC	GTT	TCG	CTG	GAT	GAC	GGC	GGT	GCC	GCC	1182
Asn	Val	Ala	Trp	Cys	Ser	Ile	Val	Ser	Leu	Asp	Asp	Gly	Gly	Ala	Gly	
325					330					335					340	
GGC	GGG	GGC	GGT	GGA	CTA	GGC	CAC	GAT	GGC	TCC	TTT	GAG	CGA	CGA	TCA	1230
Gly	Gly	Gly	Gly	Gly	Leu	Gly	His	Asp	Gly	Ser	Phe	Glu	Arg	Arg	Ser	
				345					350					355		
CCG	GGC	CTT	CAG	CCC	CAG	CAG	CTG	TTC	CTC	AAC	CAG	AGC	TTC	TCG	TAC	1278
Pro	Gly	Leu	Gln	Pro	Gln	Gln	Leu	Phe	Leu	Asn	Gln	Ser	Phe	Ser	Tyr	
			360					365					370			
CAT	CGC	AAC	AGT	GCG	ATC	AAA	GCC	GGT	GTG	TCA	GCC	ATC	TTC	GAC	CGC	1326
His	Arg	Asn	Ser	Ala	Ile	Lys	Ala	Gly	Val	Ser	Ala	Ile	Phe	Asp	Arg	
		375					380					385				
ATA	TTG	TCG	GAG	CTG	AGT	GTA	AAG	ATG	AAG	CGG	CTG	AAT	CTC	GAC	CGA	1374
Ile	Leu	Ser	Glu	Leu	Ser	Val	Lys	Met	Lys	Arg	Leu	Asn	Leu	Asp	Arg	
	390					395					400					
CGC	GAG	CTG	TCC	TGC	TTG	AAG	GCC	ATC	ATA	CTG	TAC	AAC	CCG	GAC	ATA	1422
Arg	Glu	Leu	Ser	Cys	Leu	Lys	Ala	Ile	Ile	Leu	Tyr	Asn	Pro	Asp	Ile	
405					410					415					420	
CGC	GGG	ATC	AAG	AGC	CGG	GCG	GAG	ATC	GAG	ATG	TGC	CGC	GAG	AAG	GTG	1470
Arg	Gly	Ile	Lys	Ser	Arg	Ala	Glu	Ile	Glu	Met	Cys	Arg	Glu	Lys	Val	
				425					430					435		
TAC	GCT	TGC	CTG	GAC	GAG	CAC	TGC	CGC	CTG	GAA	CAT	CCG	GGC	GAC	GAT	1518
Tyr	Ala	Cys	Leu	Asp	Glu	His	Cys	Arg	Leu	Glu	His	Pro	Gly	Asp	Asp	
			440					445					450			
GGA	CGC	TTT	GCG	CAA	CTG	CTG	CTG	CGT	CTG	CGC	CGC	TTT	GCG	ATC	GAT	1566
Gly	Arg	Phe	Ala	Gln	Leu	Leu	Leu	Arg	Leu	Arg	Arg	Phe	Ala	Ile	Asp	
		455					460					465				
CAG	CCT	GAA	GTG	CCA	GGA	TCA	CCT	GTT	CCT	CTT	CCG	CAT	TAC	CAG	CGA	1614
Gln	Pro	Glu	Val	Pro	Gly	Ser	Pro	Val	Pro	Leu	Pro	His	Tyr	Gln	Arg	
	470					475					480					

CCG GCC GCT GGA GGA GCT CTT TCT CGA GCA GCT GGA GGC GCC GCC GCC 1662
 Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly Gly Ala Ala Ala
 485 490 495 500

ACC CGG CCT GGC GAT GAA ACT GGA GTA GGG TCC CGA CTC T AAAGTCGCCC 1712
 Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg Leu
 505 510

CCGTTCTCCA TCCGAAAAAT GTTTCATTGT GATTGCGTTT GTTTGCATTT CTCCTCTCTA 1772

TCCCTACAAA AGCCCCCTAA TATTACGCAA AATGTGTATG TAATTGTTTA TTTTTTTTTT 1832

ATTACCTAAT ATTATTATTA TTATTGATAT AGAAAATGTT TTCCTTAAGA TGAAGATTAG 1892

CCTCCTCGAC GTTTATGTCC CAGTAAACGA AAAACAAACA AAATCCAAAA CTTGAAAAGA 1952

ACACAAAACA CGAACGAGAA AATGCACACA AGCAAAGTAA AAGTAAAAGT TAAACTAAAG 2012

CTAAACGAGT AAAGATATTA AAATAACGGT TAAAATTAAT GCATAGTTAT GATCTACAGA 2072

CGTATGTAAA CATACAAATT CAGCATAAAT ATATATGTCA GCAGGCGCAT ATCTGCGGTG 2132

CTGGCCCCGT TCTAAACCAA TTGTAATTAC TTTTAAACAT AAATTTACCC AAAACGTTAT 2192

CAATTAGATG CGAGATACAA AAATCACCGA CGAAAACCAA CAAAATATAT CTATGTATAA 2252

AAAATATAAG CTGCATAACA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 2304

SEQ ID NO:2 [TO BE GENERATED BY PATENTIN FROM SEQ ID NO:1]

SEQ ID NO:3

Cys - X - X - Cys - X - X - Asp* - X - Ala* - X - Gly*
 - X - Tyr* - X - X - X - X - Cys - X - X - Cys - Lys* -
 X - Phe - Phe - X - Arg* - X - X - X - X - X - X - X -
 X - X - (X - X -) Cys - X - X - X - X - X - (X - X - X
 -) Cys - X - X - X - Lys - X - X - Arg - X - X - Cys - X
 - X - Cys - Arg* - X - X - Lys* - Cys - X - X - X -
 Gly* - Met,

SEQ ID No:4 5'-AGGTCA-AGG-AGGTCA-3',

SEQ ID No:5 5'-GGGTGA-ATG-AGGACA-3',

SEQ ID No:6 5'-GGGTGA-ACG-GGGGCA-3',

SEQ ID No:7 5'-GGTTCA-CGA-GGTTCA-3',

SEQ ID No:8 5'-AGGTCA-CAGG-AGGTCA-3',

SEQ ID No:9 5'-AGGTGA-CAGG-AGGTCA-3',

SEQ ID No:10 5'-AGGTGA-CAGG-AGGACA-3',

SEQ ID No:11 5'-GGGTTA-GGGG-AGGACA-3',

SEQ ID No:12 5'-GGGTCA-TTTC-AGGTCC-3',

SEQ ID No:13 5'-AGGTCA-CCAGG-AGGTCA-3',

SEQ ID No:14 5'-AGGTGA-ACAGG-AGGTCA-3',

SEQ ID No:15 5'-GGTTCA-CCGAA-AGTTCA-3',

SEQ ID No:16 5'-GGTTCA-CCGAA-AGTTCA-3',

SEQ ID No:17 5'-AGGTCA-CTGAC-AGGGCA-3',
SEQ ID No:18 5'-GGGTCA-TTCAG-AGTTCA-3',
SEQ ID No:19 5'-AAGCTTAAG-GGTTCA-CCGAA-AGTTCA-CTCAGCTT-3',
SEQ ID No:20 5'-AAGCTTAAG-GGTTCA-CCGAA-AGTTCA-CTCGCATAGCTT-3',
SEQ ID No:21 5'-AAGCTTAAG-GGTTCA-CCGAA-AGTTCA-
CTCGCATATATTAGCTT-3',
SEQ ID NO:22 5'-AGCTCGATGG ACAAGTGCAT TGAACCCTTG AGCTACCTGT TCACGTAAC
TGGGAAC TTC GA,
SEQ ID NO:23 5'-CCTGCGCCAC GGCGGCCGCC GGAGCTGTG CCTG,
SEQ ID NO:24 5'-GTGGGTATG CGCCTCGAGT GCGTCGTCCC,
SEQ ID NO:25 5'-AGGACAAAGG TCA,
SEQ ID NO:26 ATTGGACAAGTGCATTGAACCCCTTGTCTCT
TAACCAGTTCACGTAACCTGGGAACAGAGA
SEQ ID NO:27 atgctGTGCATTGAACgctgctcga
tacgaCACGTAACCTTGcagagct
SEQ ID NO:28 atgAAGTGCATTGAACCCgctcga
tacTTCACGTAACCTTGGGcgagct
SEQ ID NO:29 TAAAGGATCTTGACCCCAATGAACTTCTTA
ATTCCTAGAACTGGGGTACTTGAAGAAT

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